WHAT IS CLAIMED IS:

1. A method for the detection of *Helicobacter pylori* (*H. pylori*) present in a sample comprising the steps of:

amplifying the polynucleic acids of the m and s regions of the vacA gene with a pair of primers, wherein one of said primers is selected from the group consisting of: SEQ ID NOS: 14-18 and, another of said primers is selected from the group consisting of SEQ ID NOS: 23-26 and 277;

hybridizing the polynucleic acids obtained with at least one probe hybridizing to a conserved region of the vacA gene and at least one probe hybridizing to a variable region of the vacA gene, thus forming hybrids;

detecting the hybrids formed; and

determining the presence or absence of *H. pylori* in a sample from the hybridization signals obtained.

2. A method according to Claim 1 wherein said primer pair for the amplification step comprises VA1F (SEQ ID NO:277) and VA1XR (SEQ ID NO:14).

3. A method according to Claim 1, wherein the hybridization step comprises hybridizing the polynucleic acids obtained in the amplification step with a set of probes, under hybridization and wash conditions, comprises at least one probe hybridizing to a conserved region of the vacA gene of *H. pylori*, and at least one vacA-derived probe selected from the group consisting of SEQ ID NOS:35-39.

4. A probe for use in a method of detecting the presence of *H. pylori*, said probe comprising a sequence selected from the group consisting of SEQ ID NOS:35-39.

5. The method of Claim 1 additionally comprising the step of releasing, isolating, or concentrating the *H. pylori* polynucleic acids in the original sample.

6. The method according to Claim 1, wherein the hybridization step is a reverse hybridization step, wherein the probes are immobilized on a solid support.

7. The method according to Claim 6, wherein said probes are immobilized as parallel lines on a solid support.

8. The method according to Claim 6, wherein said solid support is a membrane strip.

9. A kit for detecting and/or typing *H. pylori* strains in a sample liable to contain it, comprising the following components:

at least one probe selected from the group consisting of: SEQ ID NOS:1-11 and 27-39 or variants thereof, with said probe and/or other probes applied;

a buffer or components necessary to produce the buffer enabling an amplification or a hybridization reaction between said probes and the amplified products; and

a means for detecting the hybrids resulting from said hybridization.

10. The method according to Claim 9, wherein said solid support is a microtiter plate.

11. The method of Claim 1, further comprising amplifying the polynucleic acids of the cagA gene of *H. pylori* with a primer pair that amplifies a conserved region of the cagA gene of all *H.pylori* strains.

12. The method of Claim 5, wherein each primer from said primer pair comprises a primer selected from the group consisting of: SEQ ID NOS: 1, 12-13, 19-22, and 27.

13. A method according to Claim 1 for the detection and/or typing of alleles of the cagA and vacA gene of *H.pylori* present in a sample using a set of probes and/or primers specially designed to detect and/or to amplify and/or to type the said alleles, with said probes selected from the group consisting of: SEQ ID NOS: 1-11 and 27-39 and primers being selected from the group consisting of: SEQ ID NOS: 12-26 and variants thereof that can amplify said vacA or cagA region of all strains of *H.pylori*.

14. An isolated vacA polynucleotide sequence selected from the group consisting of: SEQ ID NOS: 40-91 and SEQ ID NOS: 115-276.

15. A method for the detection and/or typing of *Helicobacter pylori* (*H.pylori*) strains present in a sample comprising the steps of:

amplifying the polynucleic acids of the m and s regions of the vacA gene and a conserved region of the cagA gene, with a pair of primers, wherein said vacA primers are selected from the group consisting of: SEQ ID NOS: 14-18, 23-26, and 277;

hybridizing the polynucleic acids obtained with at least one probe hybridizing to a conserved region of the cagA gene and at least one probe hybridizing to a variable region of the vacA gene, thus forming hybrids;

detecting the hybrids formed;

detecting and/or typing *H.pylori* strains present in a sample from the differential hybridization signals obtained; wherein said typing comprises the allele-specific detection of a strain according to the vacA polynucleic acid alleles.

16. The method of Claim 11, wherein said cagA primers are selected from the group consisting of SEQ ID NOS:12-13, and 19-22.

17. The method of Claim 1, wherein said probes has compatible hybridization and wash conditions.

18. The method of Claim 11 wherein the hybridization step is a reverse hybridization step, wherein said probes are immobilized on a solid support.

19. The method according to Claim 11 wherein the polynucleic acids obtained in the amplification step are immobilized on a solid support and the subsequent hybridization step is carried out on said solid support.

20. A probe for use in a method according to Claim 11, wherein said vacA probe is selected from the group consisting of: SEQ ID NOS: 2-11 and 28-34.

21. An oligonucleotide primer, wherein said vacA primer is selected from the group consisting of SEQ ID NOS: 14-18, and 23-26.

22. A probe for detection or typing of vacA, said probe selected from the group consisting of SEQ ID NOS:2-11, and 28-39.

23. A vacA-specific oligonucleotide selected from the group consisting of SEQ ID NOS: 14-18 and 23-26.

24. A method according to claim 11 wherein at least one of said probes is selected from the group consisting of SEQ ID NOS:2-11 and 28-39 and wherein said primers are selected from the group consisting of SEQ ID NOS:14-18 and 23-26.